

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/029,905B  
Source: IFW/b  
Date Processed by STIC: 2/7/05

# ***ENTERED***

## RAW SEQUENCE LISTING

DATE: 02/07/2005

PATENT APPLICATION: US/10/029,905B

TIME: 08:37:02

Input Set : A:\1 1177 Sequence listing 3.txt

Output Set: N:\CRF4\02072005\J029905B.raw

2/7/05

## RAW SEQUENCE LISTING

DATE: 02/07/2005

PATENT APPLICATION: US/10/029,905B

TIME: 08:37:02

Input Set : A:\1\_1177 Sequence listing 3.txt

Output Set: N:\CRF4\02072005\J029905B.raw

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62 gaggatgatg atgaagagac tgctcctccc gttattgccc cgcgaccgga tcatacaaaa 480
63 tcaatttaca cacggtctgt aattgaccct gttcctgcac cagttgggtga ttcacatggt 540
64 gatggtgctg ccaagtcttt agacaaacag aaaaagaaga ctaagatgac agatgaagag 600
65 attatggaga aattaagaac tatcgtgagc ataggtgacc ctaagaaaaa atatacaaga 660
66 tatgaaaaaa ttggacaagg ggcttctggt acagttttca ctgctactga cgttgcactg 720
67 ggacaggagg ttgctatcaa acaaattaat ttacagaaac agccaaagaa ggaactgac 780
68 attaacgaga ttctggtgat gaaagaattg aaaaatccca acatcgtaa ctttttggac 840
69 agttacctgg taggagatga attgtttgtg gtcattggaat accttgctgg gaggtcactc 900
70 actgatgtgg taacagaaac gtgcatggat gaagcacaga ttgctgctgt atgcagagag 960
71 tgtttacagg cattggagtt tttacatgct aatcaagtga tccacagaga catcaaaagt 1020
72 gacaatgtac ttttggaat ggaaggatct gtttaagctca ctgactttgg tttctgtgcc 1080
73 cagatcaccct ctgagcagag caaacgcagt accatggctg gaacgccata ctggatggca 1140
74 ccagaggtgg ttacacggaa agcttatggc cctaaagtgc acatatggtc tctgggtatc 1200
75 atggctattg agatggtaga aggagagcct ccatacctca atgaaaatcc ccttagggcc 1260
76 ttgtacctaa tagcaactaa tggaacccca gaacttcaga atccagagaa actttcccca 1320
77 atatttcggg atttcttaaa tcgatgtttg gaaatggatg tggaaaaaag ggggttcagcc 1380
78 aaagaattat tacagcatcc tttcctgaaa ctggccaaac cgttatctag cttgacacca 1440
79 ctgatcatgg cagctaaaaga agcaatgaag agtaaccgtt aacatcactg ctgtggcctc 1500
80 atactctttt ttccattttc tacaagaagc ctttttagtat atgaaaatta ttactctttt 1560
81 tggggtttta agaaatggtc tgcataacct gaatgaaaga agcaaatgac tattctctga 1620
82 agacaaccaa gagaaaattg caaaaagaca agtatgactt ttatatgaac cccttcttta 1680
83 gggtcagaa ggaattgtgg actgaatcac tagccttagg tctttcagca aacagcctat 1740
84 cagggccatt tatcatgtgt gagatttgca ttttactttg ctgactttgt tgtaatatag 1800
85 ccattcatt gtccccttt 1819

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88 &lt;210&gt; SEQ ID NO: 4

89 &lt;211&gt; LENGTH: 524

90 &lt;212&gt; TYPE: PRT

91 &lt;213&gt; ORGANISM: Homo sapiens

93 &lt;400&gt; SEQUENCE: 4

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94 Met Ser Asp Asn Gly Glu Leu Glu Asp Lys Pro Pro Ala Pro Pro Val
95   1             5             10             15
97 Arg Met Ser Ser Thr Ile Phe Ser Thr Gly Gly Lys Asp Pro Leu Ser
98           20           25           30
100 Ala Asn His Ser Leu Lys Pro Leu Pro Ser Val Pro Glu Glu Lys Lys
101           35           40           45
103 Pro Arg His Lys Ile Ile Ser Ile Phe Ser Gly Thr Glu Lys Gly Ser
104           50           55           60
106 Lys Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Pro Pro Ser Asp Phe
107   65           70           75           80
109 Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe Thr
110           85           90           95
112 Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile Thr
113           100          105          110
115 Lys Leu Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu Lys
116           115          120          125
118 Phe Tyr Asp Ser Asn Thr Val Lys Gln Lys Tyr Leu Ser Phe Thr Pro
119           130          135          140
121 Pro Glu Lys Asp Gly Leu Pro Ser Gly Thr Pro Ala Leu Asn Ala Lys
122 145           150           155           160

```

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124 Gly Thr Glu Ala Pro Ala Val Val Thr Glu Glu Glu Asp Asp Asp Glu
125                               165                               170                               175
127 Glu Thr Ala Pro Pro Val Ile Ala Pro Arg Pro Asp His Thr Lys Ser
128                               180                               185                               190
130 Ile Tyr Thr Arg Ser Val Ile Asp Pro Val Pro Ala Pro Val Gly Asp
131                               195                               200                               205
133 Ser His Val Asp Gly Ala Ala Lys Ser Leu Asp Lys Gln Lys Lys Lys
134                               210                               215                               220
136 Pro Lys Met Thr Asp Glu Glu Ile Met Glu Lys Leu Arg Thr Ile Val
137 225                               230                               235                               240
139 Ser Ile Gly Asp Pro Lys Lys Lys Tyr Thr Arg Tyr Glu Lys Ile Gly
140                               245                               250                               255
142 Gln Gly Ala Ser Gly Thr Val Phe Thr Ala Thr Asp Val Ala Leu Gly
143                               260                               265                               270
145 Gln Glu Val Ala Ile Lys Gln Ile Asn Leu Gln Lys Gln Pro Lys Lys
146                               275                               280                               285
148 Glu Leu Ile Ile Asn Glu Ile Leu Val Met Lys Glu Leu Lys Asn Pro
149                               290                               295                               300
151 Asn Ile Val Asn Phe Leu Asp Ser Tyr Leu Val Gly Asp Glu Leu Phe
152 305                               310                               315                               320
154 Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu Thr Asp Val Val Thr
155                               325                               330                               335
157 Glu Thr Cys Met Asp Glu Ala Gln Ile Ala Ala Val Cys Arg Glu Cys
158                               340                               345                               350
160 Leu Gln Ala Leu Glu Phe Leu His Ala Asn Gln Val Ile His Arg Asp
161                               355                               360                               365
163 Ile Lys Ser Asp Asn Val Leu Leu Gly Met Glu Gly Ser Val Lys Leu
164                               370                               375                               380
166 Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro Glu Gln Ser Lys Arg
167 385                               390                               395                               400
169 Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Val Thr
170                               405                               410                               415
172 Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp Ser Leu Gly Ile Met
173                               420                               425                               430
175 Ala Ile Glu Met Val Glu Gly Glu Pro Pro Tyr Leu Asn Glu Asn Pro
176                               435                               440                               445
178 Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly Thr Pro Glu Leu Gln
179                               450                               455                               460
181 Asn Pro Glu Lys Leu Ser Pro Ile Phe Arg Asp Phe Leu Asn Arg Cys
182 465                               470                               475                               480
184 Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala Lys Glu Leu Leu Gln
185                               485                               490                               495
187 His Pro Phe Leu Lys Leu Ala Lys Pro Leu Ser Ser Leu Thr Pro Leu
188                               500                               505                               510
190 Ile Met Ala Ala Lys Glu Ala Met Lys Ser Asn Arg
191                               515                               520
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 50
196 <212> TYPE: DNA

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197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
202 <400> SEQUENCE: 5
203 ggggacaagt ttgtacaaaa aagcaggcta tgtctgataa cggagaactg          50
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 53
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
214 <400> SEQUENCE: 6
215 ggggaccact ttgtacaaga aagctggggt taacgggttac tcttcattgc ttc          53
218 <210> SEQ ID NO: 7
219 <211> LENGTH: 31
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
226 <400> SEQUENCE: 7
227 aagaattctc atgtctgata acggagaact g          31
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 29
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
238 <400> SEQUENCE: 8
239 tttctagaac ggttactctt cattgcttc          29
242 <210> SEQ ID NO: 9
243 <211> LENGTH: 3255
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 9
248 ggagcgcaaa tggcgtccaa ccccgaacgg ggggagattc tgctcacgga actgcagggg 60
249 gattccccgaa gtcttccggt ttctgagaat gtgagtgtctg ttcaaaaatt agacttttca 120
250 gatacaatgg tgcagcagaa attggatgat atcaaggatc gaattaagag agaaataagg 180
251 aaagaactga aaatcaaaga aggagctgaa aatctgagga aagtcacaac agataaaaaa 240
252 agtttggttt atgtagacaa ctttttgaaa aaatcaaata aaaaattaga agaactacat 300
253 cacaagctgc aggaattaaa tgcacatatt gttgtatcag atccagaaga tattacagat 360
254 tgcccaagga ctccagatac tccaaataat gacctcggtt gttctactag caacaataga 420
255 ttgaaggcct tacaaaaaca attggatata gaacttaaag taaaacaagg tgcagagaat 480
256 atgatacaga tgtattcaaa tggatcttca aaggatcgga aactccatgg tacagctcag 540
257 caactgctcc aggacagcaa gacaaaaata gaagtcatac gaatgcagat tcttcaggca 600
258 gtccagacta atgaattggc ttttgataat gcaaaacctg tgataagtc tcttgaactt 660
259 cggatggaag aattaaggca tcattttagg atagagtttg cagtagcaga aggtgcaaag 720
260 aatgtaatga aattacttgg ctcaggaaaa gtaacagaca gaaaagcact ttcagaagct 780
261 caagcaagat ttaatgaatc aagtcagaag ttggaccttt taaagtattc attagagcaa 840
262 agattaaacg aagtcoccaa gaatcatccc aaaagcagga ttattattga agaactttca 900

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263 cttgttgctg catcaccaac actaagtcca cgtcaaagta tgatatctac gcaaaatcaa 960
264 tatagtacac tatccaaacc agcagcacta acaggactct tggaagttcg tcttatgggc 1020
265 tgccaagata tcttagagaa tgtccctgga cggtcaaaag caacatcagt tgcactgcct 1080
266 ggttgagtc caagtgaac cagatcatct ttcattgagca gaacgagtaa aagtaaaagc 1140
267 ggaagtagtc gaaatcttct aaaaaccgat gacttggtcca atgatgtctg tgctgttttg 1200
268 aagctcgata atactgtggt tggccaaact agctggaaac ccattttcaa tcagtcattg 1260
269 gaccagaagt ttacactgga actggacagg tcacgtgaac tggaaatttc agttttattg 1320
270 cgtgattggc ggtctctgtg tgctgtaaaa tttctgaggt tagaagattt tttagacaac 1380
271 caacggcatg gcatgtgtct ctatttgga ccacagggtta ctttatttgc agaggttacc 1440
272 ttttttaatc cagttattga aagaagacca aaacttcaaa gacaaaagaa aattttttca 1500
273 aagcaacaag gcaaaacatt tctcagagct cctcaaatga atattaatat tgccacttgg 1560
274 ggaaggctag taagaagagc tattcctaca gtaaatcatt ctggcacctt cagccctcaa 1620
275 gctcctgtgc ctactacagt gccagtgtgt gatgtacgca tccctcaact agcacctcca 1680
276 gctagtgtat ctacagtaac caaattggac tttgatcttg agcctgaacc tcctccagcc 1740
277 ccaccacgag cttcttctct tggagaaata gatgaatctt ctgaattaag agttttggat 1800
278 ataccaggac aggattcaga gactgttttt gatattcaga atgacagaaa tagtatactt 1860
279 ccaaaatctc aatctgaata caagcctgat actcctcagt caggcctaga atatagtgg 1920
280 attcaagaac ttgaggacag aagatctcag caaagggttc agtttaaatc acaagatttc 1980
281 aggtgttgtg ctgtcttggg aagaggacat tttggaaaag tgcttttagc tgaatataaa 2040
282 aacacaaatg agatgtttgc tataaaagcc ttaaagaaaag gagatattgt ggctcgagat 2100
283 gaagtagaca gcctgatgtg tgaaaaaaga atttttgaaa ctgtgaatag tgtaaggcat 2160
284 cccttttttg tgaacctttt tgcatgtttc caaaccaaag agcatgtttg ctttgtaatg 2220
285 gaatatgtcg ccggtgggga cctaatgatg cacattcata ctgatgtctt ttctgaacca 2280
286 agagctgtat tttatgtctg ttgtgtagtt cttgggttgc agtatttaca tgaacacaaa 2340
287 attgtttata gagatttgaa attggataac ttattgctag atacagaggg ctttgtgaaa 2400
288 attgctgatt ttgggtcttg caaagaagga atgggatatg gagatagaac aagcacattt 2460
289 tgtggcactc ctgaatttct tgccccagaa gtattaacag aaacttctta tacaagggct 2520
290 gtagatttgt ggggccttgg cgtgcttata tatgaaatgc ttgttggtga gtctcccttt 2580
291 cctggtgatg atgaagagga agtttttgac agtattgtaa atgatgaag aaggtatcca 2640
292 aggttcttat ctacagaagc catttctata atgagaaggc tgtaagaag aaatcctgaa 2700
293 cggcgcttgc gggctagcga gaaagatgca gaggatgtaa aaaagcacc atttttccg 2760
294 ctaattgatt ggagcgtctc gatggacaaa aaagtaaagc caccatttat acctaccata 2820
295 agaggacgag aagatgttag taattttgat gatgaattta cctcagaagc acctattctg 2880
296 actccacctc gagaaccaag gatactttcg gaagaggagc aggaaatgtt cagagatttt 2940
297 gactacattg ctgatttgtg ttaagttgct agacactgag aaaccaagct gactcacaag 3000
298 aagacctctt aaaaatagca acccttcatt tgctctctgt gccaccaata gcttctgagt 3060
299 tttttgttgt tgttgttttt attgaaacac gtgaagattt gtttaaaagt accattctaa 3120
300 tacttcttca aaagtggctc ctcatgttac ttcagcgtaa atatgagcac tggaaacagt 3180
301 ttcattggag ttaagttgag tgaacatcgg ccatgaaaat ccatcacgaa tacttttgg 3240
302 tcaatagtct atttt 3255

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305 &lt;210&gt; SEQ ID NO: 10

306 &lt;211&gt; LENGTH: 984

307 &lt;212&gt; TYPE: PRT

308 &lt;213&gt; ORGANISM: Homo sapiens

310 &lt;400&gt; SEQUENCE: 10

311 Met Ala Ser Asn Pro Glu Arg Gly Glu Ile Leu Leu Thr Glu Leu Gln

312 1 5 10 15

314 Gly Asp Ser Arg Ser Leu Pro Phe Ser Glu Asn Val Ser Ala Val Gln

315 20 25 30

**VERIFICATION SUMMARY**

DATE: 02/07/2005

PATENT APPLICATION: US/10/029,905B

TIME: 08:37:03

Input Set : A:\1\_1177 Sequence listing 3.txt

Output Set: N:\CRF4\02072005\J029905B.raw